



IFWO

RAW SEQUENCE LISTING

DATE: 04/26/2004

PATENT APPLICATION: US/10/650,326A

TIME: 09:51:48

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04122004\J650326A.raw

3 <110> APPLICANT: CURIS INC. AND WASHINGTON UNIVERSITY
 5 <120> TITLE OF INVENTION: CONJOINT ADMINISTRATION OF MORPHOGENS AND ACE INHIBITORS IN
 6 TREATMENT OF CHRONIC RENAL FAILURE
 8 <130> FILE REFERENCE: JJJ-P01-599
 10 <140> CURRENT APPLICATION NUMBER: 10/650,326A
 11 <141> CURRENT FILING DATE: 2003-08-28
 13 <150> PRIOR APPLICATION NUMBER: 60/406,431
 14 <151> PRIOR FILING DATE: 2002-08-28
 16 <160> NUMBER OF SEQ ID NOS: 31
 18 <170> SOFTWARE: PatentIn version 3.2
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 139
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Homo sapiens
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 28 1 5 10 15
 31 Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser
 32 20 25 30
 35 Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
 36 35 40 45
 39 Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
 40 50 55 60
 43 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
 44 65 70 75 80
 47 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
 48 85 90 95
 51 Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
 52 100 105 110
 55 Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
 56 115 120 125
 59 Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 60 130 135
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 64 <211> LENGTH: 97
 65 <212> TYPE: PRT
 66 <213> ORGANISM: Homo sapiens
 68 <400> SEQUENCE: 2
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 71 1 5 10 15
 74 Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly
 75 20 25 30
 78 Lys His Asn Ser Ala Pro Met Phe Met Leu Asp Leu Tyr Asn Ala Met

Does Not Comply
Corrected Diskette Needed

pp 6, 9, 11-14

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Input Set : A:\SEQUENCE LISTING.txt

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79          35          40          45
82 Ala Val Glu Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro
83          50          55          60
86 Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln
87 65          70          75          80
90 Asp Ser His Phe Leu Thr Asp Ala Asp Met Val Met Ser Phe Val Asn
91          85          90          95
94 Leu
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98 <211> LENGTH: 431
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 3
104 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
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108 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
109          20          25          30
112 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
113          35          40          45
116 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
117          50          55          60
120 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
121 65          70          75          80
124 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
125          85          90          95
128 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
129          100          105          110
132 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
133          115          120          125
136 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
137          130          135          140
140 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
141 145          150          155          160
144 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
145          165          170          175
148 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
149          180          185          190
152 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
153          195          200          205
156 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
157          210          215          220
160 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
161 225          230          235          240
164 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
165          245          250          255
168 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
169          260          265          270
172 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
173          275          280          285

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Input Set : A:\SEQUENCE LISTING.txt

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176 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
177   290           295           300
180 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
181 305           310           315           320
184 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
185           325           330           335
188 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
189           340           345           350
192 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
193           355           360           365
196 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
197           370           375           380
200 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
201 385           390           395           400
204 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
205           405           410           415
208 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
209           420           425           430
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213 <211> LENGTH: 139
214 <212> TYPE: PRT
215 <213> ORGANISM: Mus musculus
217 <400> SEQUENCE: 4
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223 Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser
224           20           25           30
227 Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
228           35           40           45
231 Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
232           50           55           60
235 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
236 65           70           75           80
239 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
240           85           90           95
243 Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
244           100          105          110
247 Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
248           115          120          125
251 Arg Asn Met Val Val Arg Ala Cys Gly Cys His
252           130          135
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256 <211> LENGTH: 139
257 <212> TYPE: PRT
258 <213> ORGANISM: Homo sapiens
260 <400> SEQUENCE: 5
262 Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu
263 1           5           10           15
266 Pro Gln Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04122004\J650326A.raw

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267      20      25      30
270 His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln
271      35      40      45
274 Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala
275      50      55      60
278 Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn
279      65      70      75      80
282 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
283      85      90      95
286 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
287      100      105      110
290 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
291      115      120      125
294 Arg Asn Met Val Val Lys Ala Cys Gly Cys His
295      130      135
298 <210> SEQ ID NO: 6
299 <211> LENGTH: 139
300 <212> TYPE: PRT
301 <213> ORGANISM: Mus musculus
303 <400> SEQUENCE: 6
305 Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu
306 1      5      10      15
309 Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser
310      20      25      30
313 Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg
314      35      40      45
317 Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala
318      50      55      60
321 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn
322      65      70      75      80
325 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
326      85      90      95
329 Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
330      100      105      110
333 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
334      115      120      125
337 Arg Asn Met Val Val Lys Ala Cys Gly Cys His
338      130      135
341 <210> SEQ ID NO: 7
342 <211> LENGTH: 588
343 <212> TYPE: PRT
344 <213> ORGANISM: Drosophila melanogaster
346 <400> SEQUENCE: 7
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349 1      5      10      15
352 Ile Val Arg Val Ala Ser Thr Glu Asp Ile Ser Gln Arg Phe Ile Ala
353      20      25      30
356 Ala Ile Ala Pro Val Ala Ala His Ile Pro Leu Ala Ser Ala Ser Gly
357      35      40      45

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04122004\J650326A.raw

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360 Ser Gly Ser Gly Arg Ser Gly Ser Arg Ser Gly Gly Ala Ser Thr Ser
361      50      55      60
364 Thr Ala Leu Ala Lys Ala Phe Asn Pro Phe Ser Glu Pro Ala Ser Phe
365 65      70      75      80
368 Ser Asp Ser Asp Lys Ser His Arg Ser Lys Thr Asn Lys Lys Pro Ser
369      85      90      95
372 Lys Ser Asp Ala Asn Arg Gln Phe Asn Glu Val His Lys Pro Arg Thr
373      100      105      110
376 Asp Gln Leu Glu Asn Ser Lys Asn Met Ser Lys Gln Leu Val Asn Lys
377      115      120      125
380 Pro Asn His Asn Lys Met Ala Val Lys Glu Gln Arg Ser His His Lys
381      130      135      140
384 Lys Ser His His His Arg Ser His Gln Pro Lys Gln Ala Ser Ala Ser
385 145      150      155      160
388 Thr Glu Ser His Gln Ser Ser Ser Ile Glu Ser Ile Phe Val Glu Glu
389      165      170      175
392 Pro Thr Leu Val Leu Asp Arg Glu Val Ala Ser Ile Asn Val Pro Ala
393      180      185      190
396 Asn Ala Lys Ala Ile Ile Ala Glu Gln Gly Pro Ser Thr Tyr Ser Lys
397      195      200      205
400 Glu Ala Leu Ile Lys Asp Lys Leu Lys Pro Asp Pro Ser Thr Leu Val
401      210      215      220
404 Glu Ile Glu Lys Ser Leu Leu Ser Leu Phe Asn Met Lys Arg Pro Pro
405 225      230      235      240
408 Lys Ile Asp Arg Ser Lys Ile Ile Ile Pro Glu Pro Met Lys Lys Leu
409      245      250      255
412 Tyr Ala Glu Ile Met Gly His Glu Leu Asp Ser Val Asn Ile Pro Lys
413      260      265      270
416 Pro Gly Leu Leu Thr Lys Ser Ala Asn Thr Val Arg Ser Phe Thr His
417      275      280      285
420 Lys Asp Ser Lys Ile Asp Asp Arg Phe Pro His His His Arg Phe Arg
421      290      295      300
424 Leu His Phe Asp Val Lys Ser Ile Pro Ala Asp Glu Lys Leu Lys Ala
425 305      310      315      320
428 Ala Glu Leu Gln Leu Thr Arg Asp Ala Leu Ser Gln Gln Val Val Ala
429      325      330      335
432 Ser Arg Ser Ser Ala Asn Arg Thr Arg Tyr Gln Val Leu Val Tyr Asp
433      340      345      350
436 Ile Thr Arg Val Gly Val Arg Gly Gln Arg Glu Pro Ser Tyr Leu Leu
437      355      360      365
440 Leu Asp Thr Lys Thr Val Arg Leu Asn Ser Thr Asp Thr Val Ser Leu
441      370      375      380
444 Asp Val Gln Pro Ala Val Asp Arg Trp Leu Ala Ser Pro Gln Arg Asn
445 385      390      395      400
448 Tyr Gly Leu Leu Val Glu Val Arg Thr Val Arg Ser Leu Lys Pro Ala
449      405      410      415
452 Pro His His His Val Arg Leu Arg Arg Ser Ala Asp Glu Ala His Glu
453      420      425      430
456 Arg Trp Gln His Lys Gln Pro Leu Leu Phe Thr Tyr Thr Asp Asp Gly

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Generic sequence of morphogenic peptides
Polypeptides

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<210> SEQ ID NO 24
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<220> FEATURE:

This is not explained in <2207-2237 section. See p. 14 for error explanation.

invalid. Do you mean Tyr?

Tyr

His

Support for change in
page 40-41 for SEQ ID
24

10 854, 2201 1

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Ala

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<223> OTHER INFORMATION: Xaa is His or Arg
<400> SEQUENCE: 24

Leu	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5				10					15		
Pro	Xaa	Xaa	Xaa	Xaa	Ala	Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Pro
			20				25					30			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	His	Ala	Xaa	Xaa	Xaa	Xaa	Xaa
			35				40					45			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Cys	Xaa	Pro
			50				55					60			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65				70				75				80			
Val	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Met	Xaa	Val	Xaa	Xaa	Cys	Xaa	Cys
				85				90					95		
Xaa															

same type error in sequences 25-30
Sequences 25 through 30 have Xaa's
explained, but not "Artificial Sequence".

see p. 12

10/650, 326A. 1/2

<210> SEQ ID NO 31

<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: :

<400> SEQUENCE: 31

Gly Gly Pro Pro

1

needs explanation in L2207-L2237
section

This appeared several times in
sequences 28 and 29

1/650,326A 13

<220> FEATURE:

<221> NAME/KEY: VARIANT

<222> LOCATION: (46) .. (46)

<223> OTHER INFORMATION: Xaa is (Asn, Lys, Val, Thr or Gln)?

also, several locations for
Xaa showed "Serj" as an
amino acid represented by

Xaa (on 2237 line)

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/650,326A

DATE: 04/26/2004
TIME: 09:51:49

Input Set : A:\SEQUENCE LISTING.txt
Output Set : N:\CRF4\04122004\J650326A.raw

FYI

Please Note:

se of n and/or Xaa have been detected in the Sequence Listing. Please review the sequence Listing to ensure that a corresponding explanation is presented in the <220> o <223> fields of each sequence which presents at least one n or Xaa.

eq#:24; Xaa Pos. 2,3,4,6,7,8,11,12,13,14,15,16,18,19,20,21,23,26,28,30,31
eq#:24; Xaa Pos. 33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54
eq#:24; Xaa Pos. 55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77
eq#:24; Xaa Pos. 78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96
eq#:25; Xaa Pos. 2,3,4,5,7,8,9,11,12,13,16,17,18,19,20,21,23,24,25,26,28
eq#:25; Xaa Pos. 31,33,35,36,38,39,40,41,42,43,44,45,49,50,51,52,53,54,55
eq#:25; Xaa Pos. 56,57,58,59,60,61,62,63,64,65,68,70,71,72,73,74,75,76,77
eq#:25; Xaa Pos. 79,80,81,82,83,84,85,87,89,90,91,92,93,95,97,98,100,102
eq#:26; Xaa Pos. 2,3,4,5
eq#:27; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,18,19,20,21,22,23
eq#:27; Xaa Pos. 24,26,28,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45
eq#:27; Xaa Pos. 46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,63,65,66
eq#:27; Xaa Pos. 67,68,69,70,71,72,74,75,76,77,78,79,80,81,82,83,84,85,86
eq#:27; Xaa Pos. 87,88,89,90,91,92,93,95,97
eq#:28; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,23,24
eq#:28; Xaa Pos. 25,26,27,28,29,31,33,35,36,37,38,39,40,41,42,43,44,45,46
eq#:28; Xaa Pos. 47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65
eq#:28; Xaa Pos. 66,68,70,71,72,73,74,75,76,77,79,80,81,82,83,84,85,86,87
eq#:28; Xaa Pos. 88,89,90,91,92,93,94,95,96,97,98,100,102
eq#:29; Xaa Pos. 2,3,11,16,19,23,26,35,39,41,50,52,56,57,58,60,61,65,71,73
eq#:29; Xaa Pos. 75,80,82,84,89,96
eq#:30; Xaa Pos. 2,3

Invalid <213> Response:

se of "Artificial" only as "<213> Organism" response is incomplete,
er 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

eq#:24,25,26,27,28,29,30,31

Invalid <220> Feature(NEW RULES):

sequence(s) are missing the <220> Feature and associated headings.
se of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
:"Unknown". Please explain source of genetic material in <220> to <223>
action (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
Sec.1.823 of new Rules)

eq#:28,29,31,24,25,26,27,30

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/650,326A

DATE: 04/26/2004

TIME: 09:51:49

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04122004\J650326A.raw

L:2438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
M:341 Repeated in SeqNo=24
L:2838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
M:341 Repeated in SeqNo=25
L:2893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:3345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
M:341 Repeated in SeqNo=27
L:3380 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3712 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3828 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
M:341 Repeated in SeqNo=28
L:4008 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:4010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
M:341 Repeated in SeqNo=29
L:4051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:4060 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial
L:4060 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial
L:4060 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:4060